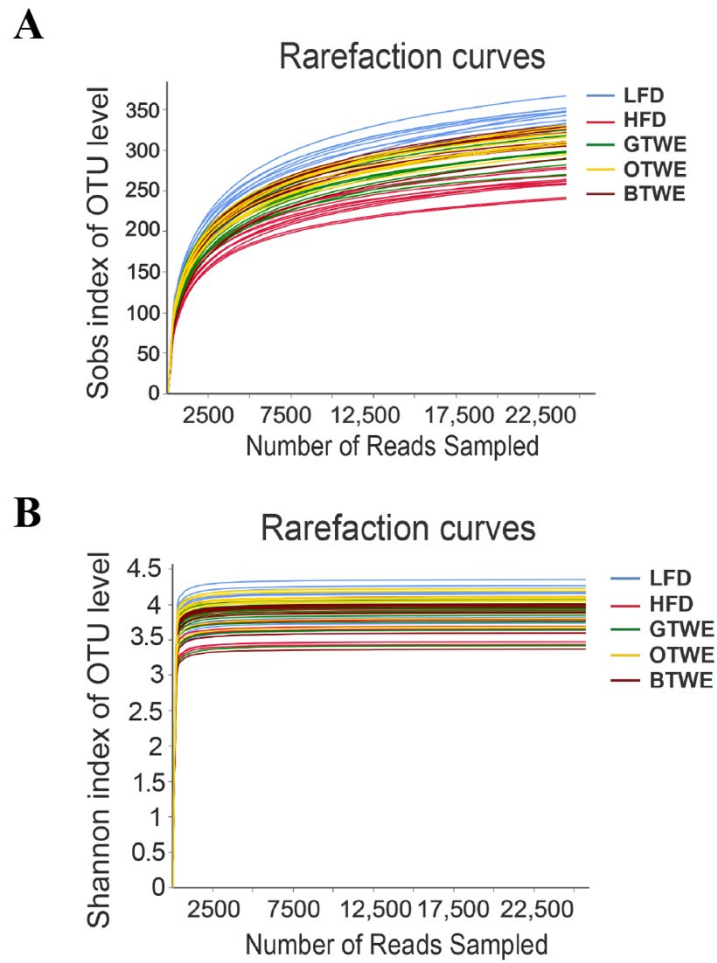


## Supporting Information

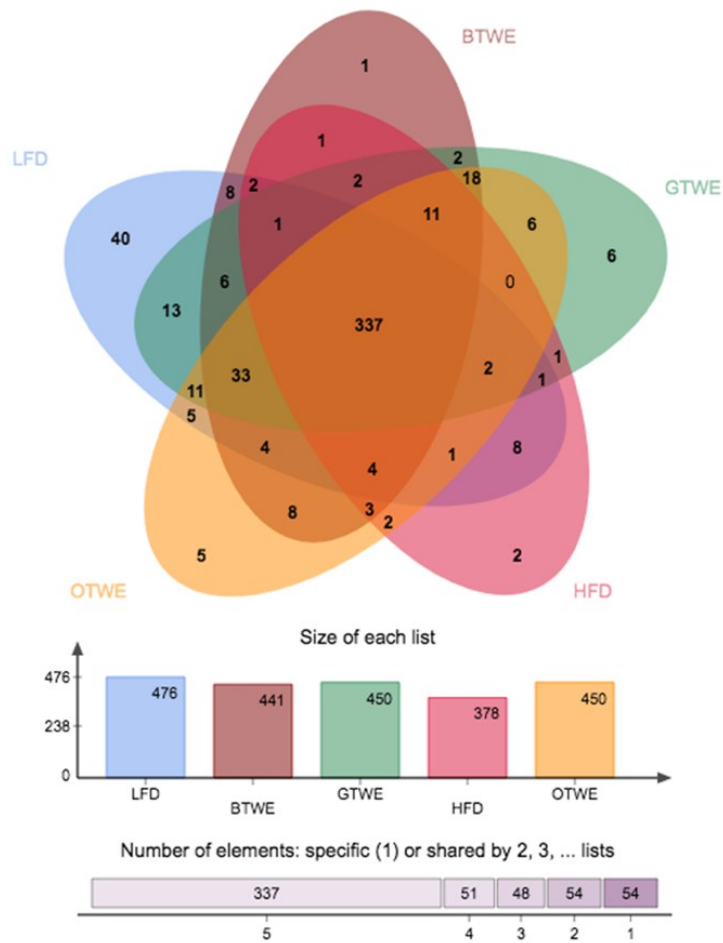
**Table S1.** Diet compositions

	LFD	HFD	GTWE	BTWE	OTWE
Ingredients (g)					
Corn starch	600.2	346.0	346.0	346.0	346.0
Gelatin	20.0	20.0	20.0	20.0	20.0
Casein	140.0	140.0	140.0	140.0	140.0
Sucrose	100.0	59.0	59.0	59.0	59.0
Powdered cellulose	50.0	50.0	50.0	50.0	50.0
Lard	40.0	171.0	171.0	171.0	171.0
AIN 76 Mineral Mix	35.0	35.0	35.0	35.0	35.0
AIN 93 Vitamin Mix	10.0	10.0	10.0	10.0	10.0
Choline Bitartrate	2.5	2.5	2.5	2.5	2.5
DL-Methionine	2.3	2.3	2.3	2.3	2.3
Cholesterol	0.0	8.4	8.4	8.4	8.4
GTWE	-	-	8.4	-	-
BTWE	-	-	-	8.4	-
OTWE	-	-	-	-	8.4
Total energy, KJ	3850	3850	3850	3850	3850
Calculated energy content, KJ/g	3.85	4.56	4.51	4.51	4.51
Energy %					
Carbohydrates	72.7	43.1	43.1	43.1	43.1
Protein	16.9	16.9	16.9	16.9	16.9
Fat	9.4	40.0	40.0	40.0	40.0

Mice were fed with low fat diet (LFD), high fat diet (HFD), and HFD supplemented with 1% of green tea (GTWE), oolong tea (OTWE), and black tea (BTWE) diets.

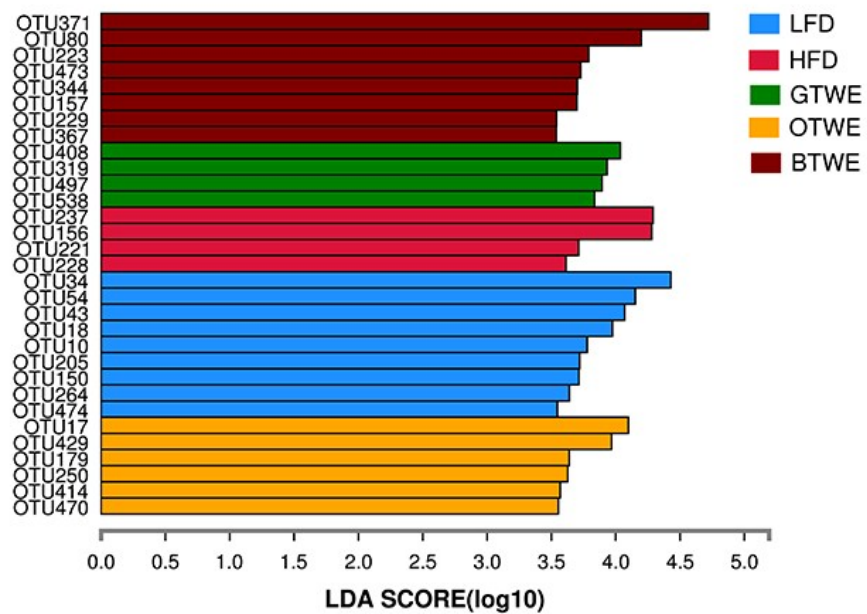


**Figure S1.** Alpha diversity analysis of fecal samples for mice fed with low fat diet (LFD), high fat diet (HFD), and HFD supplemented with green tea (GTWE), oolong tea (OTWE), and black tea (BTWE) diets. A) Rarefaction analysis (Sobs index). B) Rarefaction analysis (Shannon index).



**Figure S2.** Quantitative comparisons of bacterial OTUs among the five groups fed one of the five diets, a low fat diet (LFD), a high fat diet (HFD), and a HFD supplemented with green tea (GTWE), oolong tea (OTWE), and black tea water extracts (BTWE). The number in the overlapped ellipses indicated the OTUs shared among different groups. Total abundances of each group were analyzed to assess changes in gut microbiota.

### LefSe Bar



**Figure S3.** Linear discriminant analysis (LDA) coupled with effect size (LEfSe) analysis among all groups. Threshold of LDA = 3.5. The enriched taxa are displayed with a positive LDA score. Only taxa meeting an LDA score threshold  $\geq 3.5$  are listed.

Table S2. Taxonomic information of 31 key OTUs.

OTU	Phylum	Class	Order	Family	Genus
OTU371	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_S24-7_group	<i>norank_f__Bacteroidales_S24-7_group</i>
OTU80	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_S24-7_group	<i>norank_f__Bacteroidales_S24-7_group</i>
OTU17	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Lachnospiraceae_NK4A136_group</i>
OTU34	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Faecalibaculum</i>
OTU54	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_S24-7_group	<i>norank_f__Bacteroidales_S24-7_group</i>
OTU473	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>
OTU237	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>[Eubacterium]_coprostanoligenes_group</i>
OTU408	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>
OTU497	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	<i>Bilophila</i>
OTU429	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Lachnospiraceae_NK4A136_group</i>
OTU319	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Rikenellaceae_RC9_gut_group</i>
OTU414	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium_9</i>
OTU221	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>norank_f__Lachnospiraceae</i>
OTU223	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>Romboutsia</i>
OTU228	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_S24-7_group	<i>norank_f__Bacteroidales_S24-7_group</i>
OTU156	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>
OTU250	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_S24-7_group	<i>norank_f__Bacteroidales_S24-7_group</i>
OTU229	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Rikenella</i>
OTU179	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>
OTU43	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	<i>Bifidobacterium</i>
OTU18	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU344	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>
OTU264	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Acetatifactor</i>
OTU367	Firmicutes	Clostridia	Clostridiales	Clostridiales_vadinBB60_group	<i>norank_f__Clostridiales_vadinBB60_group</i>
OTU538	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium_9</i>
OTU205	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Lachnospiraceae_NK4A136_group</i>
OTU157	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Turicibacter</i>
OTU10	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>
OTU470	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Roseburia</i>
OTU150	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>
OTU474	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>